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HPV 45 L1 Nucleotide Sequence Alignment

45 L1 wt	(1)	ATGGCTTGTGGCGGCCTAGTGACAGTACGGTATATCTTCCACCACTTC
45 L1 R	(1)A.A..ATC....TC...T..C..CT.G.....A..
45 L1 wt	(51)	TGTGCCAGAGTTGTCAACACTGATGATTATGTGTCTGCACAAGCATAT
45 L1 R	(51)	...C..T.....C.....C..C..C..CA.A..CTC...C.
45 L1 wt	(101)	TTTACCATGCAGGCAGTCCCGATTATTAACGTAGGCAATCCATATTT
45 L1 R	(101)	.C.....C..T..TTC....A....G..G.....C..T..C.....C..C
45 L1 wt	(151)	AGGGTTGTACCTAGTGGTGCAGGTAATAAACAGGCTTCTAAGGTATC
45 L1 R	(151)	..A..C..C..ATCC.....T.....C..G..A.....A.....C..
45 L1 wt	(201)	CGCATATCAGTATAGGGTGTAGAGTAGCTTGCCCCATCCTAATAAAT
45 L1 R	(201)	T..T..C..A..C..A..C..C.....C.....A..C..A..C..G..
45 L1 wt	(251)	TTGGATTACCTGATTCTACTATATAATCCTGAAACACAACGTTGGTT
45 L1 R	(251)	.C..T..G..A..C.....C..C..C..A.....T...A.A.....C
45 L1 wt	(301)	TGGGCATGTGTAGGTATGGAAATTGGCGTGGCAGCCTTAGGTATTGG
45 L1 R	(301)C..C.....C..A.A..T..A..A..G.....C..
45 L1 wt	(351)	CCTAAGTGGCCATCCATTITATAATAAAATTGGATGATACAGAAAGTGCTC
45 L1 R	(351)	TT.GTC...T..C.....C..C..C..G.....C..C..C..TCC....
45 L1 wt	(401)	ATGCAGCTACAGCTGTTATTACGCAGGATGTTAGGGATAATGTGTCAGTT
45 L1 R	(401)	.C..T.....T.....C..C..T..A..C..C..A..C..C..C..T..C
45 L1 wt	(451)	GATTATAAGCAAACACAGCTGTGTATTTAGGTTGTACCTGCTATTGG
45 L1 R	(451)	..C..C.....C..AT.....C..G.....C..A.....C..
45 L1 wt	(501)	TGAGCACTGGGCCAAGGGCACACTTGTAAACCTGCACAATTGCAACCTG
45 L1 R	(501)	...A.....T.....T..CT.G.....G..A..T.....A..
45 L1 wt	(551)	GTGACTGTCTCCTTGGAACTAAAAACACCATTATTGAGGATGGTGAT
45 L1 R	(551)A..A.....T.G..G.....T..C..C..A..C.....C

FIG. 1A

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45 L1 wt	(601)	ATGGTGGATAACAGGTTATGGGGCAATGGATTTAGTACATTGCAGGATAC
45 L1 R	(601)T..C..T.....C..T..T.....C..CTCC..CC.....C..
45 L1 wt	(651)	AAAGTGCAGGGTTCCATTAGACATTGTCAATCCATCTGTAAATATCCAG
45 L1 R	(651)	T.....T..A.....G.....C.....T.....G..C....
45 L1 wt	(701)	ATTATTTGCAAATGTCTGCTGATCCATGGGGATTCTATGTTTTTGC
45 L1 R	(701)	.C..C.....C.....C..A..C..T..C.....C..C..T
45 L1 wt	(751)	CTACGCCGTGAACAACGTGTTGCAAGACATTTTGGAAATAGGGCAGGTGT
45 L1 R	(751)	T.GA.AA.A.....T...C..T.....C..C.....C..A..T.....
45 L1 wt	(801)	TATGGGTGACACAGTACACTACAGACCTATATATTAAAGGCACTAGCGCTA
45 L1 R	(801)	C.....T..T..A..T...T.G..C..C..G..T..CTCT....
45 L1 wt	(851)	ATATGCGTGAACACCCTGGCAGTTGTGTATTCCCTCTCCAGTGGC
45 L1 R	(851)	.C...A.A.....T..A..TTCC.....C..C..T..A.....ATC...T
45 L1 wt	(901)	TCTATTACTACTCTGATTCTCAATTATTAATAAGCCATTGGTTACA
45 L1 R	(901)C.....C..C.....G..C..C.....C.....G..
45 L1 wt	(951)	TAAGGCCAGGGCATAACAATGGTATTGTTGGCATAATCAGTTGGT
45 L1 R	(951)	C.....T..A..T..C.....C.....C.....C..C..A.....C.
45 L1 wt	(1001)	TTACTGTAGTGGACACTACCCGCAGTACTAACATTATGTGCCTCT
45 L1 R	(1001)	.C..C..C..T.....A.ATC.....C..G..C..G.....T...
45 L1 wt	(1051)	ACACAAAATCCTGTGCCAATACATATGATCCTACTAACATTAAAGCACTA
45 L1 R	(1051)	..T.....C..A..T.....C..T..C..C..A..C.....C.....
45 L1 wt	(1101)	TAGTAGACATGTGGAGGAATATGATTACAGTTATTTCAGTTGTGCA
45 L1 R	(1101)	CTCC.....C..C.....C..C..G..A..C..C..A.....T.
45 L1 wt	(1151)	CTATTACTTAACGTGAGGGTTATGTCATATCCATAGTATGAATAGT
45 L1 R	(1151)C..C..G..C..T..A..C.....C..C..T..CTC.....CTCC
45 L1 wt	(1201)	AGTATATTGAAAATTGGAATTGGTGTACCTCCACCACTACTACAAG
45 L1 R	(1201)	TC...C.....C.....C..C.....T..A.....A..C..CTC

FIG. 1B

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45 L1 wt	(1251)	TTTAGTGGATACATATCGTTTGCAATCAGTTGCTGTTACCTGTCAAA
45 L1 R	(1251)	C..G..T..C..T..CA.A..C..C.....T..C.....C..T.....
45 L1 wt	(1301)	AGGATACTACACCTCCAGAAAAGCAGGATCCATATGATAAATTAAAGTTT
45 L1 R	(1301)C..C..T..A.....A..C.....C..C..G..G.....C
45 L1 wt	(1351)	TGGACTGTTGACCTAAAGGAAAAATTTCTCCGATTGGATCAATATCC
45 L1 R	(1351)T.G.....G..C..T....C....C.....C..
45 L1 wt	(1401)	CCTTGGTCGAAAGTTTTAGTTCAAGCGTCTGCTGCTGGTTACGTCGTAGGCCTACCA
45 L1 R	(1401)	AT.G...A.....C..G.....A....T..GA.A....A..A..T.
45 L1 wt	(1451)	TAGGACCTCGTAAGCGTCTGCTGCTCCACGTCTACTGCATCTAGGCCT
45 L1 R	(1451)	.C..T..A.....A.A..A.....T..C....T....A..A
45 L1 wt	(1501)	GCCAAACGTGTACGTACGTAGTAAAAATAA (SEQ ID NO:3)
45 L1 R	(1501)	..T..G.....CA.A..CA.ATCC..G..G... (SEQ ID NO:1)

FIG.1C

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Synthetic HPV 45 L1 Nucleotide and Amino Acid Sequences

	M A L W R P S D S T V Y L P P P S
1	ATGGCTTTGT GGAGACCATC TGACTCTACT GTCTACTTGC CACCACCATC
	TACCGAAACA CCTCTGGTAG ACTGAGATGA CAGATGAACG GTGGTGGTAG
	V A R V V N T D D Y V S R T S I F
51	TGTCGCTAGA GTCGTCAACA CTGACGACTA CGTCTCCAGA ACCTCCATCT
	ACAGCGATCT CAGCAGTTGT GACTGCTGAT GCAGAGGTCT TGGAGGTAGA
	Y H A G S S R L L T V G N P Y F
101	TCTACCACGC TGTTCTTCC AGATTGTTGA CTGTCGGTAA CCCATACTTC
	AGATGGTGCG ACCAAGAAGG TCTAACAACT GACAGCCATT GGGTATGAAG
	R V V P S G A G N K Q A V P K V S
151	AGAGTCGTCC CATCCGGTGC TGGTAACAAG CAAGCTGTTC CAAAGGTCTC
	TCTCAGCAGG GTAGGCCACG ACCATTGTTTC GTTCGACAAG GTTTCCAGAG
	A Y Q Y R V F R V A L P D P N K F
201	TGCTTACCAA TACAGAGTCT TCAGAGTCGC TTTGCCAGAC CCAAACAAGT
	ACGAATGGTT ATGTCTCAGA AGTCTCAGCG AAACGGTCTG GGTTTGTCA
	G L P D S T I Y N P E T Q R L V
251	TCGGTTTGCC AGACTCTACT ATCTACAAACC CAGAAACTCA AAGATTGGTC
	AGCCAAACGG TCTGAGATGA TAGATGTTGG GTCTTGAGT TTCTAACCAAG
	W A C V G M E I G R G Q P L G I G
301	TGGGCATGCG TCGGTATGGA AATCGGTAGA GGTCAACCAT TGGGTATCGG
	ACCCGTACGC AGCCATACCT TTAGCCATCT CCAGTTGGTA ACCCATAGCC
	L S G H P F Y N K L D D T E S A H
351	TTTGTCTGGT CACCCATTCT ACAACAAGTT GGACGACACC GAATCCGCTC
	AAACAGACCA GTGGGTAAAGA TGTGTTCAA CCTGCTGTGG CTTAGGCGAG
	A A T A V I T Q D V R D N V S V
401	ACGCTGCTAC TGCTGTCATC ACTCAAGACG TCAGAGACAA CGTCTCTGTC
	TGCGACGATG ACGACAGTAG TGAGTTCTGC AGTCTCTGTT GCAGAGACAG
	D Y K Q T Q L C I L G C V P A I G
451	GACTACAAGC AAACCCAATT GTGTATCTTG GGTTGTGTCC CAGCTATCGG
	CTGATGTTCG TTTGGGTTAA CACATAGAAC CCAACACAGG GTCGATAGCC
	E H W A K G T L C K P A Q L Q P G
501	TGAACACTGG GCTAAGGGTA CCTTGTGTAA GCCAGCTAA TTGCAACCAG
	ACTTGTGACC CGATTCCCATT GGAACACATT CGGTCGAGTT AACGTTGGTC

FIG.2A

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	D C P P L E L K N T I I E D G D
551	GTGACTGTCC ACCATTGGAA TTGAAGAAC A CTATCATCGA AGACGGTGAC CACTGACAGG TGGTAACCTT AACTTCTTGT GATAGTAGCT TCTGCCACTG
	M V D T G Y G A M D F S T L Q D T
601	ATGGTTGACA CTGGTTACGG TGCTATGGAC TTCTCCACCC TGCAGGACAC TACCAA GTGACCAATGCC ACGATACTG AAGAGGTGGG ACGTCCTGTG
	K C E V P L D I C Q S I C K Y P D
651	TAAGTGTGAA GTTCCATTGG ACATCTGTCA ATCTATCTGT AAGTACCCAG ATTCACACTT CAAGGTAACC TGTAGACAGT TAGATAGACA TTCATGGTC
	Y L Q M S A D P Y G D S M F F C
701	ACTACTTGCA AATGTCCGCT GACCCATACG GTGACTCTAT GTTCTTCTGT TGATGAACGT TTACAGGCGA CTGGGTATGC CACTGAGATA CAAGAAGACA
	L R R E Q L F A R H F W N R A G V
751	TTGAGAAAGAG AACAAATTGTT CGCTAGACAC TTCTGGAACA GAGCTGGTGT AACTCTTCTC TTGTTAACAA GCGATCTGTG AAGACCTTGT CTCGACCACA
	M G D T V P T D L Y I K G T S A N
801	CATGGGTGAC ACTGTTCCAA CTGACTTGTA CATCAAGGGT ACCTCTGCTA GTACCCACTG TGACAAGGTT GACTGAACAT GTAGTTCCA TGGAGACGAT
	M R E T P G S C V Y S P S P S G
851	ACATGAGAGA AACTCCAGGT TCCTGTGTCT ACTCTCCATC TCCATCTGGT TGTACTCTCT TTGAGGTCCA AGGACACAGA TGAGAGGTAG AGGTAGACCA
	S I T T S D S Q L F N K P Y W L H
901	TCTATCACTA CTTCCGACTC TCAATTGTT AACAAGCCAT ACTGGTTGCA AGATAGTGAT GAAGGCTGAG AGTTAACAAAG TTGTTCGGT A TGACCAACGT
	K A Q G H N N G I C W H N Q L F V
951	CAAGGCTCAA GGTACAAACA ACGGTATCTG TTGGCACAAC CAATTGTTCG GTTCCGAGTT CCAGTGTGTG TGCCATAGAC AACC GTGTTG GTTAAACAAAGC
	T V V D T T R S T N L T L C A S
1001	TCACCGTCGT TGACACTACC AGATCTACTA ACTTGACCTT GTGTGCTTCT AGTGGCAGCA ACTGTGATGG TCTAGATGAT TGAACCTGGAA CACACGAAGA
	T Q N P V P N T Y D P T K F K H Y
1051	ACTCAAAACC CAGTTCCAAA CACTTACGAC CCAACCAAGT TCAAGCACTA TGAGTTTG GTCAAGGTT GTGAATGCTG GGTTGGTTCA AGTTCGTGT
	S R H V E E Y D L Q F I F Q L C T
1101	CTCCAGACAC GTCGAGGAAT ACGACTTGCA ATTCACTTCA CAATTGTTGTA GAGGTCTGTG CAGCTCCTTA TGCTGAACGT TAAGTAGAAG GTTAAACACAT
	I T L T A E V M S Y I H S M N S
1151	CTATCACCTT GACCGCTGAA GTCATGTCT ACATTCACTC TATGAACCTC GATAGTGGAA CTGGCGACTT CAGTACAGGA TGTAAGTGAG ATACTTGAGG

FIG.2B

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S I L E N W N F G V P P P P T T S
1201 TCTATCTGG AAAACTGAA CTTCGGTGTT CCACCAACAC CAACCACCTC
AGATAGAACCTT TTTTGACCTT GAAGCCACAA GGTGGTGGTG GTTGGTGGAG
L V D T Y R F V Q S V A V T C Q K
1251 CTTGGTTGAC ACTTACAGAT TCGTCCAATC TGTCGCTGTC ACTTGTCAA
GAACCAACTG TGAATGTCTA AGCAGGTTAG ACAGCGACAG TGAACAGTTT
D T T P P E K Q D P Y D K L K F
1301 AGGACACCAC TCCACCAGAA AAGCAAGACC CATAKGACAA GTTGAAGTTC
TCCTGTGGTG AGGTGGTCTT TTCGTTCTGG GTATGCTGTT CAACTTCAAG
W T V D L K E K F S S D L D Q Y P
1351 TGGACTGTTG ACTTGAAGGA AAAGTTCTCT TCCGACTTGG ACCAATACCC
ACCTGACAAC TGAACCTCCT TTTCAAGAGA AGGCTGAACC TGGTTATGGG
L G R K F L V Q A G L R R R P T I
1401 ATTGGGTAGA AAGTTCTTGG TTCAAGCTGG TTTGAGACGT AGACCAACTA
TAACCCATCT TTCAAGAACCC AAGTTCGACC AAACCTTGCA TCTGGTTGAT
G P R K R P A A S T S T A S R P
1451 TCGGTCCACG TAAGAGACCA GCTGCTTCCA CTTCCACTGC TTCTAGACCA
AGCCAGGTGC ATTCTCTGGT CGACGAAGGT GAAGGTGACG AAGATCTGGT
A K R V R I R S K K * (SEQ ID NO:2)
1501 GCTAAGCGTG TCAGAATCAG ATCCAAGAAG TAA (SEQ ID NO:1)
CGATTGCGAC AGTCTTAGTC TAGGTTCTTC ATT (SEQ ID NO:8)

FIG.2C

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NORTHERN BLOT ANALYSIS OF HPV 45 L1 R.

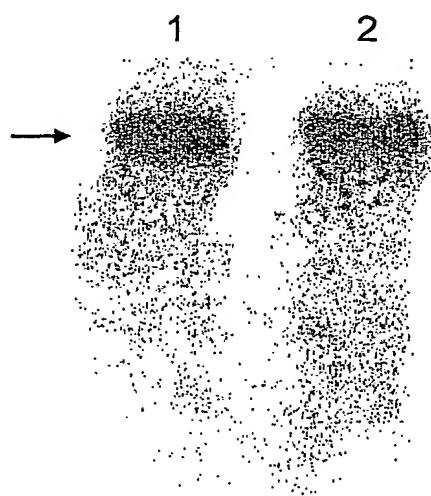


FIG.3

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WESTERN BLOT OF HPV 45 L1 wt AND
HPV 45 L1 R ISOLATES.

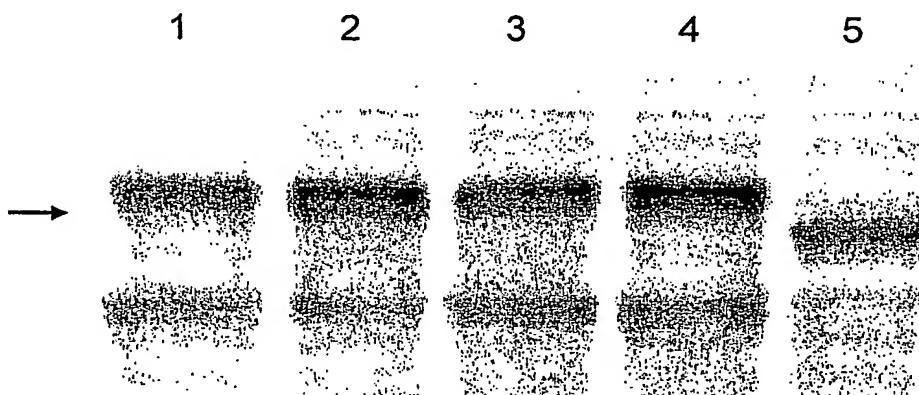


FIG.4

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ELISA ASSAY

L1 CONSTRUCT	ng VLP/mcg TOTAL PROTEIN	FOLD INCREASE OVER WILD-TYPE
45 L1 WILD-TYPE	5 ng VLP/mcg TOTAL PROTEIN	no
45 L1 ISOLATE #4	12 ng VLP/mcg TOTAL PROTEIN	2.4
45 L1 R ISOLATE #11	10 ng VLP/mcg TOTAL PROTEIN	2.0

FIG. 5

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TRANSMISSION EM OF VLPs COMPOSED OF HPV
45 L1 R PROTEIN MOLECULES.

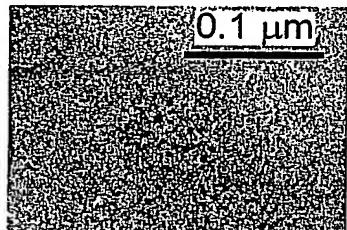


FIG.6